Abstract

NDM-1 (New Delhi metallo-β-lactamase 1) is an enzyme that is carried in certain gram negative
bacteria like E. coli and Klebsiella, and makes the bacterium resistant to the beta lactam antibiotics, including carbapenems, with the exception of the monobactam agent, aztreonam. Beta-lactamase is also known as carbapenemases, due to its resistance towards carbapenem antibiotics. Resistance to ?-lactam antibiotics mediated by metallo-?-lactamases is an increasingly worrying clinical problem. NDM-1 has been found in several clinically important carbapenem-resistant pathogens, there is a need for inhibitors of this enzyme that could protect broad spectrum antibiotics from hydrolysis and thus extend their utility. In the presented research, the 3D structure of NDM-1 protein was modeled using homology modeling by Modeller9v8. Evaluation of the constructed model is done by PROCHECK, PROSA, ERRAT and Verify3d servers. DEPTH server is used to predict active sites of Protein. Pubchem and ChEMBL, Drug Bank, and SuperNatural databases is used to find novel compounds. These compounds were docked with the modeled structure, and those showing least Binding Energy were selected. These final compounds were then tested among Online Validation Servers (Molinspiration, and OSIRIS) for Drug Likeness. Also they were validated using ADMET descriptors protocol of Accelrys Discovery Studio.

References

- BARDA Partners to Develop New Class of Antibiotic(Contract supports new antibiotic against bioterrorism threats, Gram-negative infections ) press release Sept. 6, 2011, 3:04 p. m. EDT
- PolyMedix PMX-30063 Effective Against NDM-1 Drug-Resistant Bacteria. Pharma Technology Focus. 3 May 2011

**Index Terms**

Computer Science  
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**Keywords**

Ndm-1 Metallo-?-lactamase  
Homology Modeling  
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